

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Olopade, Olufunmilayo I.
- (ii) TITLE OF INVENTION: METHYLTHIOADENOSINE PHOSPHORYLASE
COMPOSITIONS AND METHODS OF USE IN
THE DIAGNOSIS AND TREATMENT OF
PROLIFERATIVE DISORDERS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: P.O. Box 4433
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) COUNTRY: United States of America
 - (F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US Unknown
 - (B) FILING DATE: Concurrently Herewith
 - (C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/000,831
 - (B) FILING DATE: 02-JUL-1995
 - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kitchell, Barbara S.
 - (B) REGISTRATION NUMBER: 33,928
 - (C) REFERENCE/DOCKET NUMBER: ARSB:509
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (512) 418-3000
 - (B) TELEFAX: (512) 474-7577

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 122..970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| GAATTCCGCT CCGCACTGCT CACTCCCGCG CAGTGAGGTT GGCACAGCCA CCGCTCTGTG | 60 |
| GCTCGCTTGG TTCCCTTAGT CCCGAGCGCT CGCCCACTGC AGATTCCTTT CCCGTGCAGA | 120 |
| C ATG GCC TCT GGC ACC ACC ACC ACC GCC GTG AAG ATT GGA ATA ATT | 166 |
| Met Ala Ser Gly Thr Thr Thr Thr Ala Val Lys Ile Gly Ile Ile | |
| 1 5 10 15 | |
| GGT GGA ACA GGC CTG GAT GAT CCA GAA ATT TTA GAA GGA AGA ACT GAA | 214 |
| Gly Gly Thr Gly Leu Asp Asp Pro Glu Ile Leu Glu Gly Arg Thr Glu | |
| 20 25 30 | |
| AAA TAT GTG GAT ACT CCA TTT GGC AAG CCA TCT GAT GCC TTA ATT TTG | 262 |
| Lys Tyr Val Asp Thr Pro Phe Gly Lys Pro Ser Asp Ala Leu Ile Leu | |
| 35 40 45 | |
| GGG AAG ATA AAA AAT GTT GAT TGC ATC CTC CTT GCA AGG CAT GGA AGG | 310 |
| Gly Lys Ile Lys Asn Val Asp Cys Ile Leu Leu Ala Arg His Gly Arg | |
| 50 55 60 | |
| CAG CAC ACC ATC ATG CCT TCA AAG GTC AAC TAC CAG GCG AAC ATC TGG | 358 |
| Gln His Thr Ile Met Pro Ser Lys Val Asn Tyr Gln Ala Asn Ile Trp | |
| 65 70 75 | |
| GCT TTG AAG GAA GAG GGC TGT ACA CAT GTC ATA GTG ACC ACA GCT TGT | 406 |
| Ala Leu Lys Glu Glu Gly Cys Thr His Val Ile Val Thr Thr Ala Cys | |
| 80 85 90 95 | |
| GGC TCC TTG AGG GAG GAG ATT CAG CCC GGC GAT ATT GTC ATT ATT GAT | 454 |
| Gly Ser Leu Arg Glu Glu Ile Gln Pro Gly Asp Ile Val Ile Ile Asp | |
| 100 105 110 | |
| CAG TTC ATT GAC AGG ACC ACT ATG AGA CCT CAG TCC TTC TAT GAT GGA | 502 |
| Gln Phe Ile Asp Arg Thr Thr Met Arg Pro Gln Ser Phe Tyr Asp Gly | |
| 115 120 125 | |
| AGT CAT TCT TGT GCC AGA GGA GTG TGC CAT ATT CCA ATG GCT GAG CCG | 550 |
| Ser His Ser Cys Ala Arg Gly Val Cys His Ile Pro Met Ala Glu Pro | |
| 130 135 140 | |
| TTT TGC CCC AAA ACG AGA GAG GTT CTT ATA GAG ACT GCT AAG AAG CTA | 598 |
| Phe Cys Pro Lys Thr Arg Glu Val Leu Ile Glu Thr Ala Lys Lys Leu | |
| 145 150 155 | |
| GGA CTC CGG TGC CAC TCA AAG GGG ACA ATG GTC ACA ATC GAG GGA CCT | 646 |
| Gly Leu Arg Cys His Ser Lys Gly Thr Met Val Thr Ile Glu Gly Pro | |
| 160 165 170 175 | |
| CGT TTT AGC TCC CGG GCA GAA AGC TTC ATG TTC CGC ACC TGG GGG GCG | 694 |
| Arg Phe Ser Ser Arg Ala Glu Ser Phe Met Phe Arg Thr Trp Gly Ala | |
| 180 185 190 | |
| GAT GTT ATC AAC ATG ACC ACA GTT CCA GAG GTG GTT CTT GCT AAG GAG | 742 |
| Asp Val Ile Asn Met Thr Thr Val Pro Glu Val Val Leu Ala Lys Glu | |
| 195 200 205 | |
| GCT GGA ATT TGT TAC GCA AGT ATC GCC ATG GCG ACA GAT TAT GAC TGC | 790 |
| Ala Gly Ile Cys Tyr Ala Ser Ile Ala Met Ala Thr Asp Tyr Asp Cys | |

210

215

220

TGG AAG GAG CAC GAG GAA GCA GTT TCG GTG GAC CGG GTC TTA AAG ACC 838
 Trp Lys Glu His Glu Glu Ala Val Ser Val Asp Arg Val Leu Lys Thr
 225 230 235

CTG AAA GAA AAC GCT AAT AAA GCC AAA AGC TTA CTG CTC ACT ACC ATA 886
 Leu Lys Glu Asn Ala Asn Lys Ala Lys Ser Leu Leu Leu Thr Thr Ile
 240 245 250 255

CCT CAG ATA GGG TCC ACA GAA TGG TCA GAA ACC CTC CAT AAC CTG AAG 934
 Pro Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys
 260 265 270

AAT ATG GCC CAG TTT TCT GTT TTA TTA CCA AGA CAT TAAAGTAGCA 980
 Asn Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
 275 280

TGGCTGCCCA GGAGAAAAGA AGACATTCTA ATTCCAGTCA TTTTGGGAAT TCCTGCTTAA 1040

CTTGAAAAAA ATATGGGAAA GACATGCAGC TTTCATGCCC TTGCCTATCA AAGAGTATGT 1100

TGTAAGAAAG ACAAGACATT GTGTGTATTA GAGACTCCTG AATGATTTAG ACAACTTCAA 1160

AATACAGAAG AAAAGCAAAT GACTAGTAAA CATGTGGGAA AAAATATTAC ATTTTAAGGG 1220

GGAAAAAAA AACCCACCA TTCTCTTCTC CCCCTATTAA ATTTGCAACA ATAAAGGGTG 1280

GAGGGTAATC TCTACTTTCC TATACTGCCA AAGAATGTGA GGAAGAAATG GGACTCTTTG 1340

GTTATTTATT GATGCGACTG TAAATTGGTA CAGTATTTCT GGAGGGCAAT TTGGTAAAAT 1400

GCATCAAAAG ACTTAAAAAT ACGGACGTCC TTTGGTGCTG GGAAGCTCTAC ATCTAGCAAT 1460

TTCTCTTTAA AACCATATCA GAGATGCATA CAAAGAATTA TATATAAAGA AGGGTGTTTA 1520

ATAATGATAG TTATAATAAT AAATAATTGA AACAATCTGA ATCCCTTGCA ATTGGAGGTA 1580

AATTATGTCT TAGTTATAAT CTAGATTGTG AATCAGCCAA CTGAAAATCC TTTTTCGATA 1640

TTTCAATGTC CTAAAAAGAC ACGGTTGCTC TATATATGAA GTGAAAAAAG GATATGGTAG 1700

CATTTTATAG TACTAGTTTT GCTTTAAAAT GCTATGTAAA TATACAAAAA AACTAGAAAG 1760

AAATATATAT AACCTTGTTA TTGTATTTGG GGGAGGGATA CTGGGATAAT TTTTATTTTC 1820

TTTGAATCTT TCTGTGTCTT CACATTTTTC TACAGTGAAT ATAATCAAAT AGTAAAGGGC 1880

CGTAAAAATA AAAGTGGATT TAGAAAGATC CAGTTCTTGA AAACACTGTT TCTGGTAATG 1940

AAGCAGAATT TAAGTTGGTA ATATTAAGGT GAATGTCATT TAAGGGAGTT ACATCTTTAT 2000

TCTGCTAAAG AAGAGGATCA TTGATTTCTG TACAGTCAGA ACAGTACTTG GGTGTGCAAC 2060

AGCTTTCTGA GAAAAGCTAG GTGTATAATA GTTTAACTGA AAGTTTAACT ATTTAAAAGA 2120

CTAAATGCAC ATTTTATGGT ATCTGATATT TTAAAAAGTA ATGTGAGCTT CTCCTTTTAA 2180

TGAGTTAAAT TATTTTATAC GAGTTGGTAA TTTGTGCCTT TTAATAAAGT GGAAGCTTGC 2240

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Gly | Thr | Thr | Thr | Thr | Ala | Val | Lys | Ile | Gly | Ile | Ile | Gly | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Gly | Thr | Gly | Leu | Asp | Asp | Pro | Glu | Ile | Leu | Glu | Gly | Arg | Thr | Glu | Lys | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Val | Asp | Thr | Pro | Phe | Gly | Lys | Pro | Ser | Asp | Ala | Leu | Ile | Leu | Gly | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Lys | Ile | Lys | Asn | Val | Asp | Cys | Ile | Leu | Leu | Ala | Arg | His | Gly | Arg | Gln | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| His | Thr | Ile | Met | Pro | Ser | Lys | Val | Asn | Tyr | Gln | Ala | Asn | Ile | Trp | Ala | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Leu | Lys | Glu | Glu | Gly | Cys | Thr | His | Val | Ile | Val | Thr | Thr | Ala | Cys | Gly | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Leu | Arg | Glu | Glu | Ile | Gln | Pro | Gly | Asp | Ile | Val | Ile | Ile | Asp | Gln | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Phe | Ile | Asp | Arg | Thr | Thr | Met | Arg | Pro | Gln | Ser | Phe | Tyr | Asp | Gly | Ser | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| His | Ser | Cys | Ala | Arg | Gly | Val | Cys | His | Ile | Pro | Met | Ala | Glu | Pro | Phe | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Cys | Pro | Lys | Thr | Arg | Glu | Val | Leu | Ile | Glu | Thr | Ala | Lys | Lys | Leu | Gly | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Leu | Arg | Cys | His | Ser | Lys | Gly | Thr | Met | Val | Thr | Ile | Glu | Gly | Pro | Arg | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Phe | Ser | Ser | Arg | Ala | Glu | Ser | Phe | Met | Phe | Arg | Thr | Trp | Gly | Ala | Asp | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Val | Ile | Asn | Met | Thr | Thr | Val | Pro | Glu | Val | Val | Leu | Ala | Lys | Glu | Ala | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Gly | Ile | Cys | Tyr | Ala | Ser | Ile | Ala | Met | Ala | Thr | Asp | Tyr | Asp | Cys | Trp | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Lys | Glu | His | Glu | Glu | Ala | Val | Ser | Val | Asp | Arg | Val | Leu | Lys | Thr | Leu | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Lys | Glu | Asn | Ala | Asn | Lys | Ala | Lys | Ser | Leu | Leu | Leu | Thr | Thr | Ile | Pro | |

Gln Ile Gly Ser Thr Glu Trp Ser Glu Thr Leu His Asn Leu Lys Asn
260 265 270
Met Ala Gln Phe Ser Val Leu Leu Pro Arg His
275 280

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGTGAAGG TGAGA

15

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTTAGATTG GAATA

15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTGGCAAGG TTAAT

15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCAGCCAT CTGAT

15

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTGCAAGGT ATGG

14

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATAGGCAT GGA

13

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGAGAGAGG TGTGT

15

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCTAGGTTC TTATA

15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGGAAGCAG TAGGT

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTCTAGGTTT CGGTG

15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACCTGAAGG TAAGT

15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCCAGAATA TGGCC

15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTGCTTTTTT AACTC

15